

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 02:49:34 ; Search time 68 seconds

(without alignments)
- 891.799 Million cell updates/sec

Title: US-09-308-829-2

Perfect score: 1232

Sequence: 1 MKKINIKIVITVILISF.....KDNRIIMKNFSDIYLEK 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1187	96.3	235	16	08NXX2
2	1051	85.3	206	2	054512
3	556	45.1	232	16	0990N1
4	393.5	31.9	240	16	08P2R5
5	387.5	31.5	234	16	08K807
6	386.5	31.4	234	2	093RR9
7	386.5	31.4	234	2	08G9K7
8	370.5	30.1	210	2	09K2G9
9	289	23.5	226	2	09S1H8
10	288	23.4	233	16	08N289
11	287.5	23.3	209	2	09LAC6
12	287.5	23.3	209	2	09LAC1
13	286.5	23.3	209	2	09LAC4
14	285.5	23.2	209	2	09R005
15	285.5	23.2	209	2	09LAD0
16	285.5	23.2	209	2	09LAD9

17	285.5	23.2	209	2	09LAD8	09lad8 streptococc
18	285	23.1	209	2	09LAD1	09lad1 streptococc
19	284.5	23.1	209	2	09LAE0	09lae0 streptococc
20	283.5	23.0	209	2	09LAC5	09lac5 streptococc
21	283.5	23.0	209	2	09LAD7	09lad7 streptococc
22	283	23.0	209	2	09LAD2	09lad2 streptococc
23	282.5	22.9	209	2	09LAC9	09lac9 streptococc
24	281.5	22.8	209	2	09LAC8	09lac8 streptococc
25	279.5	22.7	209	2	09LAD5	09lad5 streptococc
26	279.5	22.7	209	2	09LAD4	09lad4 streptococc
27	279	22.6	233	16	099XW1	099xw1 streptococc
28	278.5	22.6	209	2	09LAC3	09lac3 streptococc
29	278.5	22.6	209	2	09LAD6	09lad6 streptococc
30	273	22.2	256	2	09S1H9	09s1h9 streptococc
31	272.5	22.1	209	2	09LAD3	09lad3 streptococc
32	271.5	22.0	209	2	09LAC7	09lac7 streptococc
33	270	21.9	256	2	09X9R8	09x9r8 streptococc
34	226	18.3	240	16	09F0L7	09f0l7 staphylococc
35	226	18.3	240	16	08NXX5	08nx5 staphylococc
36	219	17.8	241	16	053585	053585 staphylococc
37	219	17.8	256	2	08VLM7	08v1w7 staphylococc
38	216	17.5	242	2	093CC6	093cc6 staphylococc
39	216	17.5	242	16	08NVM3	08nvm3 staphylococc
40	211.5	17.2	237	16	08P0R9	08p0r9 streptococc
41	210	17.0	238	2	08L3E1	08l3e1 streptococc
42	210	17.0	239	2	09E2W7	09e2w7 staphylococc
43	210	17.0	239	16	099T47	099t47 staphylococc
44	210	17.0	251	16	08K6K5	08k6k5 streptococc
45	202.5	16.4	259	16	0938J1	0938j1 streptococc

ALIGNMENTS

RESULT 1

ID	Q8NRX2	PRELIMINARY:	PRT:	235 AA.
AC	Q8NRX2:			
DT	01-OCT-2002 (TREMblrel. 22, Created)			
DT	01-OCT-2002 (TREMblrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMblrel. 23, Last annotation update)			
DE	Exotoxin C.			
GN	SPEC OR SPYMI8.0778.			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
CC	NCBI_taxid=186103;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MGAS8232 / Serotype M18;			
RX	MEDLINE=21927593; PubMed=11917108;			
RA	Smoot J.C., Bairdian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,			
RA	Sylyva G.L., Sturdevant D.E., Ricklets S.M., Porcella S.F.,			
RA	Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,			
RA	Kapur V., Daly J.A., Yeasy L.G., Musser J.M.;			
RT	"Genome sequence and comparative microarray analysis of serotype M18			
RT	group A Streptococcus strains associated with acute rheumatic fever			
RT	outbreaks";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
RL	EMBL; AE010008; AL97445.1; -			
DR	InterPro: IPR006177; Bctrl_tox.			
DR	InterPro: IPR006123; Staph/Strep_toxin.			
DR	InterPro: IPR006126; Staph/Strep_tox.			
DR	InterPro: IPR006173; Staph_tox_DB.			
DR	InterPro: IPR01123; Staph_tox_C; 1.			
DR	PIfam; PF02876; Staph_tox_C; 1.			
DR	PRINTS; PR00279; BACTRLTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 235 AA; 27372 MW; 53BD041B958C65B CRC64;			

Query Match 96.3%; Score 1187; DB 16; Length 235;

Best Local Similarity 97.4%; Pred. No. 3 5e-75;
Matches 229; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 MKKINIKIVFITYVILISTFYFYHOSDKSDISNVKSDLYAYTTTPYKDCRYNFST 60
DB 1 MKKINIKIVFITYVILISTFYFYHOSDKSDISNVKSDLYAYTTTPYKDCRYNFST 60
OY 61 THTLNDIDOKYKGDYISSEMSYEAQKFRDHDVDFGLTYILNSHTGEYIGGITPA 120
DB 61 THTLNDIDOKYKGDYISSEMSYEAQKFRDHDVDFGLTYILNSHTGEYIGGITPA 120
OY 121 QNNKYNHKLGLNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKYLMDNYKIYATSPY 180
DB 121 QNNKYNHKLGLNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKYLMDNYKIYATSPY 180
OY 181 VSGRIETGKDGKHEQIDLFDSPNECTRSIDIFAKYKDNRIIMKNFSHFDIYLEK 235
DB 181 VSGRIETGKDGKHEQIDLFDSPNECTRSIDIFAKYKDNRIIMKNFSHFDIYLEK 235

RESULT 2

ID 054512 PRELIMINARY: PRT: 206 AA.
AC 054512:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE T1M1 ISOLATE SME88 SPEC (Exotoxin C) (Fragment).
CN SPEC.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T1M1;
RA MEDLINE-94253335; PubMed-8195383;
RA Norrby-Teglund A., Holm S.E., Norgren M.;
RT "Detection and nucleotide sequence analysis of the spec gene in
RT Swedish clinical group A streptococcal isolates.";
RL J. Clin. Microbiol. 32:705-709(1994).
RN [2]
RP SEQUENCE OF 14-169 FROM N.A.
RC STRAIN-D976;
RA Beesen D.E., Izzo M.W., Fiorentino T.R., Carling R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U02560; AAB59978.2; -
DR EMBL: AF055700; AAD11626.1; -
DR HSSP: P13380; IAN8.
DR InterPro: IPR006177; Bcrl-tox.
DR InterPro: IPR006123; Stap/Strep_toxin.
DR InterPro: IPR006126; Stap/Strep_tox.
DR InterPro: IPR006173; Stapl_tox_OB.
DR Pfam: PF01123; Stap_strp_toxin; 1.
DR Pfam: PF02876; Stap_strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPL_STRP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPL_STRP_TOXIN_2; 1.
FT NON_TER 1
FT VARIANT 33 33 N -> D.
FT NON_TER 206 206
SQ SEQUENCE 206 AA; 23955 MW; 14DB9CF06C46C9CB CRC64;

Query Match 85.3%; Score 1051; DB 2; Length 206;
Best Local Similarity 99.0%; Pred. No. 8.6e-66;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 26 QSSKSDISNVKSDLYAYTTTPYKDCRYNFSTHTLNDIDOKYKGDYISSEMSYE 85
DB 6 KSDSKDISNVKSDLYAYTTTPYKDCRYNFSTHTLNDIDOKYKGDYISSEMSYE 65

OY 86 ASQKFRDHDVDFGLTYILNSHTGEYIGGITPAQNNKYNHKLGLNLFISGESQONLN 145
DB 66 ASQKFRDHDVDFGLTYILNSHTGEYIGGITPAQNNKYNHKLGLNLFISGESQONLN 125
OY 146 KIIIEKDIYVFOEIDFKIRKYLMDNYKIYATSPYSGRIETGKDGKHEQIDLFDSPN 205
DB 126 KIIIEKDIYVFOEIDFKIRKYLMDNYKIYATSPYSGRIETGKDGKHEQIDLFDSPN 185
OY 206 GTRSDIFAKYKDNRIIMKNF 226
DB 186 GTRSDIFAKYKDNRIIMKNF 206

RESULT 3

ID 0990N1 PRELIMINARY: PRT: 232 AA.
AC 0990N1:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Putative exotoxin (Superantigen) (Streptococcal pyrogenic exotoxin J)
DE (Exotoxin J precursor).
CN SPEC OR SPY0436.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE-21192684; PubMed-11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC PubMed-11179302;
RA McCormick J.K., Pragman A.A., Stolpa J.C., Leung D.Y.,
RA Schlievert P.M.;
RT "Functional Characterization of Streptococcal Pyrogenic Exotoxin J, a
RT Novel Superantigen.";
RN Infect. Immun. 69:1381-1388(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE-99093428; PubMed-9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE-21259899; PubMed-11359827;
RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
RT "Immunological and biochemical characterization of streptococcal
RT pyrogenic exotoxins I and J (Spe-I and Spe-J) from Streptococcus
RT pyogenes.";
RL J. Immunol. 166:6711-6719(2001).
DR EMBL: AE006504; AAK33456.1; -
DR EMBL: AF321000; AAG59819.1; -
DR EMBL: AF438523; AAL31570.1; -
DR HSSP: P13380; IAN8.
DR InterPro: IPR006123; Stap/Strep_toxin.
DR InterPro: IPR006173; Stapl_tox_OB.
DR Pfam: PF01123; Stap_strp_toxin; 1.
DR Pfam: PF02876; Stap_strp_tox_C; 1.
DR PROSITE: PS00278; STAPL_STRP_TOXIN_1; 1.
DR SIGNAL: Complete proteome.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 232 AA; 27171 MW; 15D1774768EB2789 CRC64;

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Query Match      45.1%; Score 556; DB 16; Length 232;
Best Local Similarity 48.3%; Pred. No. 2,6e-31;
Matches 113; Conservative 39; Mismatches 76; Indels 6; Gaps 3;

OY 1 MKKINIKIVFIIIVILISTYFTYHQSDDSKDISNVKSDLLVAYTTPYDKDCRVNFTSTHT 60
DB 1 MKRI-----IKTIILVIIIFHFGYSVKSDDS-ENIKDVKQLQVLVAYEIIIPVDTCNIDILT 55
OY 61 THTLINDTQKRGADYIISSEMSYEASOKFRDHDVDFGLFYLLNSHTGEYITGGITPA 120
DB 56 THDYIDISSYKKNKNEFSDSEVSYITTKFKNOKVNFGLPYIFTRDYVYIIGGVTPS 115
OY 121 QN-KNVNKKLGNLFISGEQQNLNNKILTEKDIYTFQCEIDFKIRKYLMDYKTIYDASP 179
DB 116 VNSNSESKTYGNLLIDGVQOKLILNPRIKIDKPIFTIOEPFKIRQYLMQTKIYDNPSP 175
OY 180 YVSGRIEIGTKDGHQIDLPDSPNEGTRSDIFAKYKDNRIINKNKSFHDYIL 233
DB 176 YIKQLEIAIINGNHESFNLYDATSSSTRSDIFKKYKDNKTIINMKDFSHFDIYL 229

RESULT 4
ID 08P2R5 PRELIMINARY; PRT; 240 AA.
AC 08P2R5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Exotoxin G.
GN SPBG OR SPYM18_0201.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Studevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE009699; AAL9695.1; -.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_toxOB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
KM SEQUENCE 240 AA; 28071 MW; 1D90199A92A10900 CRC64;

Query Match      31.9%; Score 393.5; DB 16; Length 240;
Best Local Similarity 37.0%; Pred. No. 5,5e-20;
Matches 87; Conservative 56; Mismatches 85; Indels 7; Gaps 5;

OY 6 IIRIVFIIIVLISFTFY--HOSDSKKDISNVKSDLLVAYTTPYDKDCRVNFTSTHT 63
DB 5 ILTFENILITILISCVSYGSQLAYADENLKDRLSRLEFYVNTIPCDYENVEIAFVTTNS 64
OY 64 LNIIDTQYRGK-DYIISSEMSYEASOKFRDHDVDFGLFYLLNSHTGEYITGGITPAON 122
DB 65 IHIMTKOKRSECLIVYDSIVSLGITDOFIKGDVDFGLPYNFSPPYDNIYGVIVKSN 124
OY 123 --KNVNHKKLGNLFISGEQQNLNNKILTEKDIYTFQCEIDFKIRKYLMDYKTIYDASP 180
DB 125 QGNK-SLOFVGILNQDKEITYLPSEAVRIKKKQFTLQEFDFKIRKFLMEKYNIVDSERY 183

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OY 181 VSGRIEIGTKDGHQIDLPDSPNE-GTRSDIFAKYKDNRIINKNKSFHDYILE 234
DB 184 TSGSLFATKDSKHVEYDLFNKDKLLSRDSFFKRYKDNKIFNSEIISHFDIYLK 238

RESULT 5
ID 08K807 PRELIMINARY; PRT; 234 AA.
AC 08K807;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Pyrogenic exotoxin G.
GN SPBG OR SPYM3_0155.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; AE014139; AAM78762.1; -.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_toxOB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
KM SEQUENCE 234 AA; 27282 MW; AD12C5F8B06F3D CRC64;

Query Match      31.5%; Score 387.5; DB 16; Length 224;
Best Local Similarity 37.6%; Pred. No. 1,4e-19;
Matches 86; Conservative 54; Mismatches 82; Indels 7; Gaps 5;

OY 12 ITIVILISTYFTY--HOSDSKKDISNVKSDLLVAYTTPYDKDCRVNFTSTHTLINDTQ 69
DB 5 ILTIILISCVSYGSQLAYADENLKDRLSRLEFYVNTIPCDYENVEIAFVTTNSIHINTK 64
OY 70 KYRGK-DYIISSEMSYEASOKFRDHDVDFGLFYLLNSHTGEYITGGITPAON--KNVN 126
DB 65 OKRSECLIVYDSIVSLGITDOFIKGDVDFGLPYNFSPPYDNIYGVIVKSNQGNK-S 123
OY 127 HKLGNLFISGEQQNLNNKILTEKDIYTFQCEIDFKIRKYLMDYKTIYDASPVSGRIE 186
DB 124 LQFVGILNQDKEITYLPSEAVRIKKKQFTLQEPDLKIRKFLMEKYNIVDSRSRTSGSLF 183
OY 187 IGTDKGHQIDLPDSPNE-GTRSDIFAKYKDNRIINKNKSFHDYILE 234
DB 184 LATDSKHVEYDLFNKDKLLSRDSFFKRYKDNKIFNSEIISHFDIYLK 232

RESULT 6
ID 093RR9 PRELIMINARY; PRT; 234 AA.
AC 093RR9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Streptococcal group G pyrogenic exotoxin G (SPBG) precursor.
GN SPBG.
OS Streptococcus equisimilis.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=39086;
RA Seidel P., Gerlach D., Guenther E., Relchardt W., Straube E.,
RA Schmidt K.H.;
RT "Streptococcus dysgalactiae subsp. equisimilis can carry superantigen
RT spec like gene.";
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ294849; CAC40152.1; -.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin_1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLOTXIN.
KM Signal.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 234 AA: 27107 MW: 1170CC725B78B098 CRC64;
1 24 POTENTIAL.
25 234 SPEG.
27107 MW: 1170CC725B78B098 CRC64;

Query Match 31.4%; Score 386.5; DB 2; Length 234;
Best Local Similarity 35.3%; Pred. No. 1.6e-19;
Matches 83; Conservative 54; Mismatches 91; Indels 7; Gaps 4;

OY 3 KINIKIVFIIITVILISYFTYHOSDSKDISNVKSDLLVATITPPYKDCRVNFSSTH 62
DB 2 KIKTLKIIILSNVLSYSGSKLVY---ADEILKDLKASIRFAYDVPLEYENVEITFVTN 57
OY 63 TLNIDT-OKYRGKDYIISSEMSYEASOKFKRBDHYDVGELFYILNSHTGEYIGITPAQ 121
DB 58 NIHINTGKKSGCVLYVDISVLSGITDNFIMGKADVGLPNFSSPVDNIYGGVYKHS 117
OY 122 NKNVNH-KLGNLFISGESQONLNKKIILEKDIYTFQEDIFKIRKYLMDNKIYDANSPY 180
DB 118 DDQQTOSLQFVGLNODGETSLPSYTLIIKHQFTLQEFDFKIRKFLMETYSIYDSERY 177
OY 181 VSGRIEIGTKGKHQIDLPDSPNCGT-RSDIFPAKYKONRIINKNFSHPDIYLE 234
DB 178 ISGSFELATKDSKHIEVDLFNKDKLGRNRFKRYKRONKVFNSSEISHFDIYLK 232

RESULT 7
O8G9K7 PRELIMINARY; PRT; 234 AA.
AC O8G9K7
ID O8G9K7
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Superantigen SPEG.
GN SPEG.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G 39072;
RA MEDLINE=22269278; PubMed=12381468;
RA Sachse S., Seidel P., Gerlach D., Guenther E., Roedel J., Straube E.,
RA Schmidt K.H.;
RT "Superantigen like gene(s) in human pathogenic Streptococcus
RT dysgalactiae subsp. equisimilis: Genomic localization of the gene
RT encoding streptococcal pyrogenic exotoxin G (Speg).";
RL FEMS Immunol. Med. Microbiol. 34:159-167 (2002).
DR EMBL; AJ489606; CAD33902.1; -.
DR EMBL; AJ489606; CAD33902.1; -.
SQ SEQUENCE 234 AA: 27149 MW: 24A890372B817887 CRC64;

Query Match 31.4%; Score 386.5; DB 2; Length 234;
Best Local Similarity 35.3%; Pred. No. 1.6e-19;
Matches 83; Conservative 54; Mismatches 91; Indels 7; Gaps 4;
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OY 3 KINIKIVFIIITVILISYFTYHOSDSKDISNVKSDLLVATITPPYKDCRVNFSSTH 62
DB 2 KIKTLKIIILSNVLSYSGSKLVY---ADEILKDLKASIRFAYDVPLEYENVEITFVTN 57
OY 63 TLNIDT-OKYRGKDYIISSEMSYEASOKFKRBDHYDVGELFYILNSHTGEYIGITPAQ 121
DB 58 NIHINTGKKSGCVLYVDISVLSGITDNFIMGKADVGLPNFSSPVDNIYGGVYKHS 117
OY 122 NKNVNH-KLGNLFISGESQONLNKKIILEKDIYTFQEDIFKIRKYLMDNKIYDANSPY 180
DB 118 DDQQTOSLQFVGLNODGETSLPSYTLIIKHQFTLQEFDFKIRKFLMETYSIYDSERY 177
OY 181 VSGRIEIGTKGKHQIDLPDSPNCGT-RSDIFPAKYKONRIINKNFSHPDIYLE 234
DB 178 ISGSFELATKDSKHIEVDLFNKDKLGRNRFKRYKRONKVFNSSEISHFDIYLK 232

RESULT 8
O9K2G9 PRELIMINARY; PRT; 210 AA.
AC O9K2G9
ID O9K2G9
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Exotoxin G (Fragment).
GN SPEG.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11227, and 1/5045;
RA Proft T.K., Weller K.D., Martin D., Fraser J.D.;
RT "Multiple alleles of streptococcal pyrogenic exotoxin G gene.";
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233455; AAF60292.1; -.
DR EMBL; AF233454; AAF60291.1; -.
DR HSSP; P13380; IAN8.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin_1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLOTXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON-TER
FT SEQUENCE 210 AA: 24684 MW: FEEESD36EB079209 CRC64;

Query Match 30.1%; Score 370.5; DB 2; Length 210;
Best Local Similarity 38.9%; Pred. No. 1.9e-18;
Matches 81; Conservative 47; Mismatches 75; Indels 5; Gaps 4;

OY 31 KDISNVKSDLLVATITPPYKDCRVNFSSTHITLNDTQYRGK-DYIISSEMSYEASOK 89
DB 2 ENLMDLKRSLRFAYNIPCDYENVEIAFVTNSHIMTKQKRSCLLYVDISVLSGITDQ 61
OY 90 FKRDHYDVGELFYILNSHTGEYIGITPAQN--NKNVNH-KLGNLFISGESQONLNKKI 147
DB 62 FIKBDKDVDFGLPNFSSPVDNIYGGIVKHSNOGNK-SLQFVGLNODGETFLPSEVV 120
OY 148 ILEKDIYTFQEDIFKIRKYLMDNKIYDANSPYVSGRIEIGTKGKHQIDLPSPNCG 206
DB 121 RIKKKQTLQFDFDKIRKFLMETKYNIDSESRVTSGLFLATKDSKHIEVDLFNKDKL 180
OY 207 TRSDIFPAKYKONRIINKNFSHPDIYLE 234
DB 181 SRDSFFKRYKONKTFNSSEISHFDIYLK 208

RESULT 9
O9S1H8
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ID	09S1H8	PRELIMINARY;	PRT:	256 AA.
AC	09S1H8:			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)		
DE	SpeX protein precursor.			
GN	SpeX.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=12714, type 12;			
RA	MEDLINE=20374978; PubMed=10913699;			
RA	Geslach D., Fleischner B., Wagner M., Schmidt K.H., Vettermann S.,			
RT	Reichardt W.;			
RT	"Purification and Biochemical Characterization of a Basic Superantigen			
RL	(SPEX/SME23).";			
RL	FEMS Microbiol. Lett. 188:153-163(2000).			
DR	EMBL: AJ245405; CAB51744.1; ..			
DR	HSSP: P13163; 1SXT.			
DR	InterPro: IPR006177; Bcetr1_tox.			
DR	InterPro: IPR006123; Scap/Strp_toxin.			
DR	InterPro: IPR006173; Scaph_tox_OB.			
DR	Pfam: PF011123; Scap_Strp_toxin; 1.			
DR	Pfam: PF02876; Scap_Strp_tox_C; 1.			
DR	PRINTS: PR00279; BACTRLOXIN.			
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Signal.			
FT	1	47		
SEQUENCE	256 AA: 29706 MW: 8730DBAEFBE6DC332 CRC64;			

Query Match	23.5%	Score 289:	DB 2:	Length 256;
Best Local Similarity	32.2%	Pred. 0.1.le-12:		
Matches	78;	Conservative	41;	Mismatches 105; Indels 18; Gaps 6
QY	1	MKNIINIKIVITIVILISTFYFYHQSDSKDISNVKSDLLYAVYITFYEDYKDCRVNFST	60	
Db	24	MKTKRLIFSFISFIALISIRVFGLEVNNSILRNI-----YSTIYEYSDIYIDFKT	76	
QY	61	THRLINDITOKY--RGKDYIISSEMSYASQKFKRDHVDYFGL---FYILNSTHTEYI	113	
Db	77	SH--NLVYTKKLDVBDARDPFINSEMEDEYAADFCKTGDKIAFVSVPEDMNVLSKGVATY	134	
QY	114	YGGITPFAONNVNKKLLGNLFISGESQONLNKKILLEDIYTFQEDIDKIRKYLMDNKI	173	
Db	135	YGGITPPOKLOLYLRISLVNLWINGQISVPYNIEISTNTTGTATQEDIDKVRFFLIAHQ	194	
QY	174	YDATSPYSGRIEIGTKDKNHE-QHDLDPDSNEGSRSDLPFAKYKNRILNNKMFSPHIY	232	
Db	195	YSSGSSYSKGRLVPHHTNDNSPKYSFDLF-YVGYRDKESIFVYKKNKSFNIDKIGHLDIE	253	
QY	233	LE 234		
Db	254	ID 255		
RESULT	10			
Q8NZ89				
ID	Q8NZ89	PRELIMINARY;	PRT:	233 AA.
AC	Q8NZ89;			
DT	01-OCT-2002 (TREMBlrel. 22, Created)			
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Mitogenic exotoxin Z.			
GN	SMZ OR SPY18_2064.			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
CC	Streptococcus			
OX	NCBI_TaxID=186103;			
RP	SEQUENCE FROM N.A.			
RN	(1)			

RC STRAIN-MGAS8232 / Serotype M18:
RX MEDLINE-21927593; PubMed-11917108:
RA Smoot J.C., Barbhan K.D., Van Gompel J.T., Smoot L.M., Chaussee M.S.,
RA Sylla G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.:
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A *Streptococcus* strains associated with acute rheumatic fever
RT outbreaks.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RL EMBL; AE010110; AAL98535.1; -
DR InterPro: IPR006177; Bcrlr toxin.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF011123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_tox_C_1.
DR PRINTS: PR002479; BACTRITOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 233 AA; 26859 MW; 23B07CC9C06AE866 CRC64;

Query Match	Similarity	23.4%	Score 288;	DB 16;	Length 233;
Best Local	Similarity	30.6%	Pred. No. 1,2e-12;		
Matches	74;	Conservative	47;	Mismatches 103;	Indels 18; Gaps 6

OY	1	MKNIINIKIVETITVILISTYFTYHOSDSKDISNVKSDLLYATITPYDYKDCRVNFST	60
DB	1	MKTKTLIFSEFSIFAIISRPVIGLEVNNISILRNITYSTIM-----YKSDTVIDERT	53
OY	61	THTLNIDIPQK---RGKDYITSSSEHSYASQKFKRDDHVDVFGL----FYILNSTGELY	113
DB	54	SH--LVLYKKLDVARDARDFINSEMEDXYAANDFKGDKITAMSVFDMNYSLEGVIAVT	111
OY	114	YGIPTPAONNNVNHKLLNFISESGOONLNKKILLEKDIOTYFOEIDFKIRKLYMDNYKI	173
DB	112	YGMPTPYKTSIPKPIIPVNMINGQISVPYNEISTNTTYTAGSIDDLKVRFLAQCQL	171
OY	174	YDASPYVSGRIEICTKQKHE-QIDFDSPEGTRSDIFPAKYKNRIITMKNFSFDIY	232
DB	172	YSSGSSYKSGKLVFHTNDNSDKYSLDF--YVGYRDKESIFKVKYKDKMSFNIIDKIGHLDIE	230
OY	233	LE 234	
DB	231	ID 232	

RESULT	11
ID	O9LAC6
AC	O9LAC6;
DT	01-OCT-2000 (TREMBlrel. 15, Created)
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE	Mitogenic exotoxin Z-20 (Fragment).
GN	SMEZ-20.
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=1314;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=10989;
RX	MEDLINE=20273982; PubMed=10811869;
RA	Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA	Fraser J.D.;
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT	Mosaic Structure, and Significant Antigenic Variation.";
RL	J. Exp. Med. 191:1765-1776(2000).
DR	EMBL; AF143670; AAF66669.1; -.
DR	HSEF; F13163; ISXT.
DR	InterPro; IPR006123; Staph/Strep_toxin.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	Pfam; PF01123; Staph_stp_toxin; 1.

DR pfam: PF02876; Staph_strep_tox_C: 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24100 MW; 53049A11599BEA68 CRC64;

Query Match 23.3%; Score 287.5; DB 2; Length 209;
 Best Local Similarity 34.7%; Pred. No. 1.le-12;
 Matches 69; Conservative 35; Mismatches 84; Indels 11; Gaps 5;

QY 44 YTTIPYDKDRVNFSTHTLNIIDTQK---RGKDYIISSEMSYEASQKFRDDHVDVFG 100
 ID 09LAC4 PRELIMINARY; PRT; 209 AA.
 AC 09LAC4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin 2-22 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24071 MW; 3611E7C456DEDE8 CRC64;

RESULT 12

Q9LAE1 PRELIMINARY; PRT; 209 AA.
 ID 09LAE1
 AC 09LAE1
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin 2-3 (Fragment).
 DE SMEZ-3.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=11681;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143653; AAF66654.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24071 MW; 3611E7C456DEDE8 CRC64;

Query Match 23.3%; Score 287.5; DB 2; Length 209;
 Best Local Similarity 33.7%; Pred. No. 1.le-12;
 Matches 67; Conservative 37; Mismatches 84; Indels 11; Gaps 5;

QY 44 YTTIPYDKDRVNFSTHTLNIIDTQK---RGKDYIISSEMSYEASQKFRDDHVDVFG 100
 ID 09ROQ5 PRELIMINARY; PRT; 209 AA.
 AC 09ROQ5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 22, Last annotation update)
 DE Mitogenic exotoxin 2 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24071 MW; 3611E7C456DEDE8 CRC64;

QY 216 KDNRIIMKNFSHFDIYLE 234
 ID 09LAC4 PRELIMINARY; PRT; 209 AA.
 AC 09LAC4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin 2-22 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24075 MW; 3611E7C456DEDE8 CRC64;

RESULT 13

Q9LAC4 PRELIMINARY; PRT; 209 AA.
 ID 09LAC4
 AC 09LAC4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin 2-22 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24075 MW; 3611E7C456DEDE8 CRC64;

Query Match 23.3%; Score 286.5; DB 2; Length 209;
 Best Local Similarity 34.2%; Pred. No. 1.3e-12;
 Matches 68; Conservative 37; Mismatches 83; Indels 11; Gaps 5;

QY 44 YTTIPYDKDRVNFSTHTLNIIDTQK---RGKDYIISSEMSYEASQKFRDDHVDVFG 100
 ID 09ROQ5 PRELIMINARY; PRT; 209 AA.
 AC 09ROQ5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 22, Last annotation update)
 DE Mitogenic exotoxin 2 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24075 MW; 3611E7C456DEDE8 CRC64;

RESULT 14

Q9ROQ5 PRELIMINARY; PRT; 209 AA.
 ID 09ROQ5
 AC 09ROQ5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 22, Last annotation update)
 DE Mitogenic exotoxin 2 (Fragment).
 DE SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1;
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR pfam: PF01123; Staph_strep_toxin; 1.
 DR pfam: PF02876; Staph_strep_tox_C; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 DR NON_TER 1
 FT SEQUENCE 209 AA; 24075 MW; 3611E7C456DEDE8 CRC64;

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